STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 140618

To: Karen A Lacourciere **Location:** REM/2D15/2C18 **Art Unit:** 1635 **Tuesday, December 21, 2004** **Case Serial Number:** 08/765244	**From:** Beverly Shears **Location:** Remsen Bldg. RM 1A54 **Phone:** 571-272-2528 beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches - 10/8/04

All of the sequence databases on the ABSS have been updated. A change has occurred in the protein databases.

- Two protein databases, SPTREMBL and SwissProt, are now produced as a single, merged database called UniProt.
- Results from UniProt have the file extension **.rup**.
- Sequences in UniProt are identified by the same ID that had been used in SPTREMBL or SwissProt.
- In instances where the database curators have determined that an SPTREMBL record and a SwissProt record represent the same sequence, the two records have been merged into one. Both IDs are present in the record. Any differences found between the two sequences are recorded in the FT (feature table) fields.

If you have any questions regarding these changes or your results, please contact any STIC searcher.

STIC-Biotech/ChemLib 140618 LATE

From: Lacourciere, Karen
Sent: Thursday, December 16, 2004 4:03 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search Request 08/765,244

Please search SEQ ID NO:1 and 22 for 08/765,244 in the amino acid databases. Please search the commercial databases and the pending files (interference) Thank-you!

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

1: 41 AA
pro 22-43 AA

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

Date completed: _____
Searcher: Beverly e2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search
_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors
_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

TO-1590 (9-90)

Lacourciere

FILE 'REGISTRY' ENTERED AT 10:19:53 ON 21 DEC 2004
L13 11 S MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS/SQSP

FILE 'CAPLUS' ENTERED AT 10:21:48 ON 21 DEC 2004
L14 6 S L13

L14 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 12 Jun 2003
ACCESSION NUMBER: 2003:448590 CAPLUS
Correction of: 2003:177122
DOCUMENT NUMBER: 139:31810
Correction of: 138:216594
TITLE: Differentially expressed nucleic acids and their encoded proteins associated with pain and their use in screening for regulatory agents
INVENTOR(S): Woolf, Clifford; D'Urso, Donatella; Befort, Katia; Costigan, Michael
PATENT ASSIGNEE(S): The General Hospital Corporation, USA; Bayer AG
SOURCE: PCT Int. Appl., 1017 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003016475	A2	20030227	WO 2002-XC25765	20020814
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2003016475	A2	20030227	WO 2002-US25765	20020814
WO 2003016475	A3	20040910		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:		
US 2001-312147P	P	20010814
US 2001-346382P	P	20011101
US 2001-333347P	P	20011126
WO 2002-US25765	A	20020814

AB The present invention relates to human and rat nucleic acid sequences which are related to pain and which are differentially expressed during

pain. The nucleic acids are differentially expressed by at least ±1.4-fold in any or all of the following conditions using the Affymetrix human U95, murine U74 and rat U34 GeneChip arrays: axotomy, spared nerve injury, chronic construction, spinal segmental nerve lesion, and inflammatory pain models. The invention further relates to methods of identifying nucleic acid sequences which are differentially expressed during pain, microarrays comprising such differentially expressed sequences, and methods of screening agents for the ability to regulate the expression of such differentially expressed sequences. [This abstract record is one of seven records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **540832-88-0**
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; differentially expressed nucleic acids and their encoded proteins associated with pain and their use in screening for regulatory agents)

L14 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 15 Sep 1995
ACCESSION NUMBER: 1995:792849 CAPLUS
DOCUMENT NUMBER: 123:220296
TITLE: Method for preparation of conjugates of signal peptides and nucleic acid fragments and their use in targeting nucleic acids in cells and cell organelles
INVENTOR(S): Seibel, Peter; Seibel, Andrea
PATENT ASSIGNEE(S): Germany
SOURCE: Ger., 19 pp.
CODEN: GWXXAW
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 4421079	C1	19950817	DE 1994-4421079	19940616
DE 19520815	A1	19951221	DE 1995-19520815	19950611
DE 19520815	C2	19960725		
WO 9534665	A2	19951221	WO 1995-DE775	19950611
WO 9534665	A3	19960222		
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9526679	A1	19960105	AU 1995-26679	19950611
EP 774006	A2	19970521	EP 1995-921691	19950611
R: AT, BE, CH, DE, FR, GB, IE, IT, LI, LU, NL				
US 2001008771	A1	20010719	US 1997-765244	19971030
PRIORITY APPLN. INFO.:			DE 1994-4421079	A1 19940616
			WO 1995-DE775	W 19950611

AB Linkage of a nucleic acid fragment to a signal sequence allows the transport of the nucleic acid sequence through the membrane to a specific target for use in gene therapy. In linking the nucleotide sequence to a signal peptide, natural protein transport pathways can be used for site-directed mutagenesis and for the mol. therapy of inherited diseases. The nucleic acid moiety of the conjugate may be synthesized chemical, e.g. to incorporate nuclease-resistant phosphorothioate, or by transcription. A 39 nucleotide fragment is linked to the signal sequence of the rat mitochondrial ornithine carboxylase to achieve transport across the mitochondrial membrane. The oligonucleotide forms a hairpin loop and has a 5' overhang to which further nucleic acid sequences can be linked.

IT **168147-56-6**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; method for preparation of conjugates of peptides and nucleic acid fragments and their use in targeting nucleic acids in cells and cell organelles)

L14 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 31 Oct 1987
ACCESSION NUMBER: 1987:548500 CAPLUS
DOCUMENT NUMBER: 107:148500
TITLE: Structure of the rat ornithine carbamoyltransferase gene, a large, X chromosome-linked gene with an atypical promoter
AUTHOR(S): Takiguchi, Masaki; Murakami, Takashi; Miura, Satoshi; Mori, Masataka
CORPORATE SOURCE: Med. Sch., Kumamoto Univ., Kumamoto, 862, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1987), 84(17), 6136-40
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Rat mitochondrial ornithine carbamoyltransferase (EC 2.1.3.3) is encoded by a gene located on the X chromosome and expressed specifically in the liver and small intestine; this gene was cloned and its structure determined The gene is 75 kilobases long and is split into 10 exons. The introns range in length from 85 bases to 26 kilobases. The sum of the total exons is 1.5 kilobase and occupies only 2% of the gene; this value being one of the lowest among genes heretofore reported. The 1st exon encodes most of the N-terminal presequence that functions as a mitochondrial targeting signal. Putative binding sites for the 2 substrates of the enzyme, carbamoyl phosphate and ornithine, are encoded by exons 3 and 9, resp. A set of CAAT box- and ATA box-like sequences is present ≈200 bases upstream from the 5' end of the mRNA. About 35 bases downstream from this set of putative promoter elements, and 11-nucleotide sequence around the 5' end of the mRNA reappears, as a direct repeat. This pair of direct repeats may play a role in pulling the cap site and the promoter elements together. Upstream and downstream from the 5' end of the mRNA there are several sequences that resemble the transcription factor Sp1-binding site, the enhancer core sequence, the consensus sequence for the glucocorticoid receptor-binding sites, and the putative enhancer element of the antithrombin III gene, another gene that is expressed specifically in the

liver.
IT **94949-11-8**
RL: PRP (Properties)
(amino acid sequence of)

L14 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 27 Jul 1985
ACCESSION NUMBER: 1985:417684 CAPLUS
DOCUMENT NUMBER: 103:17684
TITLE: The primary structure of the imported mitochondrial protein, ornithine transcarbamylase from rat liver: mRNA levels during ontogeny
AUTHOR(S): McIntyre, Peter; Graf, Lynda; Mercer, Julian F. B.; Wake, Samantha A.; Hudson, Peter; Hoogenraad, Nicholas
CORPORATE SOURCE: Dep. Biochem., La Trobe Univ., Bundoora, 3083, Australia
SOURCE: DNA (1985), 4(2), 147-56
CODEN: DNAADR; ISSN: 0198-0238
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Ornithine transcarbamylase [9001-69-8], one of the enzymes of the urea cycle in ureotelic organisms, is synthesized in the cytoplasm of hepatocytes as a precursor larger than the mature form found in the mitochondrial matrix. The amino acid sequence of the precursor of ornithine transcarbamylase from rat liver was deduced from the nucleotide sequence of overlapping cDNA clones spanning the complete coding region, 3'-untranslated region, and most of the 5'-untranslated region of the mRNA. The mature enzyme consists of 322 amino acids and is derived from the larger precursor by proteolytic removal of 32 amino acids from N terminus. The N-terminal extension contains 8 basic and no acidic residues. This highly basic character appears to be a feature of presequences on cytoplasmically synthesized mitochondrial proteins. A comparison of the amino acid sequence determined for the enzyme from rat with
that from human liver shows that there is a high degree of homol. between the sequences of the mature protein (93%) and relatively less homol. between the sequences of the N-terminal extension (72%). The ornithine transcarbamylase from rat liver also shows a considerable degree of amino acid homol. (44%) with the enzyme from Escherichia coli, which leads to suggestions about residues involved in substrate binding and catalysis. Ornithine transcarbamylase mRNA levels increase from .apprx.40% of adult levels at day 14 of gestation to a peak at day 20 of gestation and, after a drop around the time of birth, rise to adult levels during the 2nd wk after birth.
IT **94949-11-8**
RL: PRP (Properties)
(amino acid sequence of)

L14 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 18 May 1985
ACCESSION NUMBER: 1985:161372 CAPLUS
DOCUMENT NUMBER: 102:161372
TITLE: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylase: comparison of rat and human leader sequences and conservation of catalytic sites

AUTHOR(S): Kraus, Jan P.; Hodges, Peter E.; Williamson, Cynthia L.; Horwich, Arthur L.; Kalousek, Frantisek; Williams, Kenneth R.; Rosenberg, Leon E.
CORPORATE SOURCE: Sch. Med., Yale Univ., New Haven, CT, 06510, USA
SOURCE: Nucleic Acids Research (1985), 13(3), 943-52
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A DNA was cloned that was complementary to the mRNA encoding the precursor of ornithine transcarbamylase [9001-69-8] from rat liver. This cDNA contains the entire protein coding region of 1062 nucleotides and 86 nucleotides of 5'- and 298 nucleotides of 3'-untranslated sequences. The predicted amino acid sequence was confirmed by extensive protein sequence data. The mature rat enzyme contains the same number of amino acid residues (322) as the human enzyme, and the amino acid sequences are 93% homologous. The rat and human amino-terminal leader sequences of 32 amino acids, on the other hand, are only 69% homologous. The rat leader contains no acidic and 7 basic residues compared to 4 basic residues found in the human leader. There is complete sequence homol. (residues 58-62) among the ornithine and aspartate transcarbamylases from Escherichia coli and the rat and human ornithine transcarbamylases at the carbamyl phosphate binding site. Finally, a cysteine-containing hexapeptide (residues 268-273), the putative ornithine binding site in Streptococcus faecalis, S. faecium, and bovine transcarbamylases, is completely conserved among the 2 E. coli and the 2 mammalian transcarbamylases.

IT **95917-60-5**
RL: PRP (Properties)
(amino acid sequence of)

L14 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
ED Entered STN: 22 Mar 1985
ACCESSION NUMBER: 1985:90778 CAPLUS
DOCUMENT NUMBER: 102:90778
TITLE: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoyltransferase precursor
AUTHOR(S): Takiguchi, Masaki; Miura, Satoshi; Mori, Masataka; Tatibana, Masamiti; Nagata, Shigekazu; Kaziro, Yoshito
CORPORATE SOURCE: Sch. Med., Chiba Univ., Chiba, 280, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1984), 81(23), 7412-16
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The mRNA of rat specifying ornithine carbamoyltransferase (EC 2.1.3.3) [9001-69-8], a mitochondrial matrix enzyme, was enriched by immunopptn. of rat liver free polysomes, and recombinant plasmids were prepared from the enriched mRNA by a vector-primer method. The cDNA clones for ornithine carbamoyltransferase were identified by a hybrid-arrested translation and hybrid-selected translation. One of the clones, pOTC-1, contained a 1.6-kilobase (kb) insert and hybridized to a mRNA of .apprx.1.8 kb in rat liver. The cDNA clone was subjected to nucleotide sequence anal. The deduced amino acid sequence indicated that the ornithine carbamoyltransferase precursor [80146-82-3] consists of a mature enzyme of 322 amino acid residues and an N-terminal peptide extension (presequence) of 32 amino acid residues. The presequence contains 8 basic

amino acid residues, no acidic residues, and no hydrophobic amino acid stretch. The amino acid sequence of rat ornithine carbamoyltransferase was compared with the recently reported sequence of the human enzyme. Approx. 93% of the sequences of the mature enzyme portion are identical, whereas 69% of the presequences are identical. There are 2 highly conserved segments in the presequences of the rat and human enzymes. One of the 2 conserved segments is significantly similar to a segment of the presequence of yeast mitochondrial elongation factor EF-Tu. Apparently, the homologous segments are important for proteins that are synthesized in the cytosol to be transported into the mitochondrial matrix.

IT **94949-11-8**
RL: PRP (Properties)
(amino acid sequence of)

E27 THROUGH E30 ASSIGNED

FILE 'REGISTRY' ENTERED AT 10:22:19 ON 21 DEC 2004
L15 4 SEA FILE=REGISTRY ABB=ON PLU=ON (94949-11-8/BI OR 168147-56-6 /BI OR 540832-88-0/BI OR 95917-60-5/BI)

L16 4 L13 AND L15

L16 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2004 ACS on STN
RN **540832-88-0** REGISTRY
CN Pain-regulated protein (rat clone WO03016475-SEQID-12767) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1675: PN: WO03016475 SEQID: 12767 claimed protein
CI MAN
SQL 354

SEQ
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     51 EEIQYMLWLS ADLKFRIKQK GEYLPLLQGK SLGMIFEKRS TRTRLSTETG
    101 FALLGGHPSF LTTQDIHLGV NESLTDTARV LSSMTDAVLA RVYKQSDLDI
    151 LAKEATIPIV NGLSDLYHPI QILADYLTLQ EHYGSLKGLT LSWIGDGNNI
    201 LHSIMMSAAK FGMHLQAATP KGYEPDPNIV KLAEQYAKEN GTRLSMTNDP
    251 LEAARGGNVL ITDTWISMGQ EDEKKKRLQA FQGYQVTMKT AKVAASDWTF
    301 LHCLPRKPEE VDDEVFYSPR SLVFPEAENR KWTIMAVMVS LLTDYSPVLQ
    351 KPKF
```
HITS AT: 1-33

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:31810

L16 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2004 ACS on STN
RN **168147-56-6** REGISTRY
CN L-Cysteine, L-methionyl-L-leucyl-L-seryl-L-asparaginyl-L-leucyl-L-arginyl-L-isoleucyl-L-leucyl-L-leucyl-L-asparaginyl-L-lysyl-L-alanyl-L-alanyl-L-leucyl-L-arginyl-L-lysyl-L-alanyl-L-histidyl-L-threonyl-L-seryl-L-methionyl-L-valyl-L-arginyl-L-asparaginyl-L-phenylalanyl-L-arginyl-L-tyrosylglycyl-L-lysyl-L-prolyl-L-valyl-L-glutaminyl-L-seryl-L-glutaminyl-L-valyl-L-glutaminyl-L-leucyl-L-lysyl-L-prolyl-L-arginyl-L-α-aspartyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 1-43-Decarboxylase, ornithine [43-cysteine] (rat precursor)
CI MAN
SQL 43

SEQ 1 MLSNLRILLN KAALRKAHTS MVRNFRYGKP VQSQVQLKPR DLC
========== ========== ========== ===
HITS AT: 1-33

REFERENCE 1: 123:220296

L16 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2004 ACS on STN
RN **95917-60-5** REGISTRY
CN Carbamoyltransferase, preornithine (rat clone pRO21) (9CI) (CA INDEX NAME)
CI MAN
SQL 354

SEQ 1 MLSNLRILLN KAALRKAHTS MVRNFRYGKP VQSQVQLKGR DLLTLKNFTG
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51 EEIQYMLWLS ADLKFRIKQK GEYLPLLQGK SLGMIFEKRS TRTRLSTETG
101 FALLGGHPSF LTTQDIHLGV NESLTDTARV LSSMTDAVLA RVYKQSDLDI
151 LAKEATIPIV NGLSDLYHPI QILADYLTLQ EHYGSLKGLT LSWIGDGNNI
201 LHSIMMSAAK FGMHLQAATP KGYEPDPNIV KLAEQYAKEN STRLSMTNDP
251 LEAARGGNVL ITDTWISMGQ EDEKKKRLQA FQGYQVTMKT AKVAASDWTF
301 LHCLPRKPEE VDDEVFYSPR SLVFPEAENR KWTIMAVMVS LLTDYSPVLQ
351 KPKF
HITS AT: 1-33

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 102:161372

L16 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2004 ACS on STN
RN **94949-11-8** REGISTRY
CN Carbamoyltransferase, preornithine (rat clone pOTC-1) (9CI) (CA INDEX NAME)
CI MAN
SQL 354

SEQ 1 MLSNLRILLN KAALRKAHTS MVRNFRYGKP VQSQVQLKGR DLLTLKNFTG
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151 LAKEATIPIV NGLSDLYHPI QILADYLTLQ EHYGSLKGLT LSWIGDGNNI
201 LHSIMMSAAK FGMHLQAATP KGYEPDPNIV KLAEQYAKEN GTRLSMTNDP
251 LEAARGGNVL ITDTWISMGQ EDEKKKRLQA FQGYQVTMKT AKVAASDWTF
301 LHCLPRKPEE VDDEVFYSPR SLVFPEAENR KWTIMAVMVS LLTDYSPVLQ
351 KPKF
HITS AT: 1-33

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 107:148500

REFERENCE 2: 103:17684

REFERENCE 3: 102:90778

(FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 10:23:04 ON 21 DEC 2004)
L17 0 S L16

FILE 'HOME' ENTERED AT 10:23:13 ON 21 DEC 2004

Searcher : Shears 571-272-2528